



O I P E

RAW SEQUENCE LISTING

DATE: 05/31/2002

PATENT APPLICATION: US/10/029,180

TIME: 08:27:25

Input Set : A:\MIC-004.ST25.txt

Output Set: N:\CRF3\05312002\J029180.raw

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3 <110> APPLICANT: Cali, Brian M.
4 Holtzman, Doug
5 Madden, Kevin T.
6 Milna, G. Todd
7 Sherman, Amir
8 Silva, Jeffry C.
9 Trueheart, Josh
10 Zhang, Lixin
12 <120> TITLE OF INVENTION: Novel Regulators of Fungal Gene Expression
14 <130> FILE REFERENCE: MIC-004
16 <140> CURRENT APPLICATION NUMBER: US 10/029,180
17 <141> CURRENT FILING DATE: 2001-12-22
19 <150> PRIOR APPLICATION NUMBER: US 60/257,431
20 <151> PRIOR FILING DATE: 2000-12-22
22 <160> NUMBER OF SEQ ID NOS: 138
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37 cgcaccgacg atcctaactc ggtcaagctt ctcgagcgat acgaccagtg gtttgataac 180
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53 gcagatgaag gggccaacga agagcacacg tcttcccgcc gctcgcgcgg cgcagcagct 1140
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57 ttgaacggaa agaccaacgc tggcattcat gccccgagaa ttggacacgc atcccttgcc 1380
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59 tccccattcg ttaaataccc tgactccgat gactttggat tcggcccctc ataccttcct 1500
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62 aatggctggc ttccagtgga ccagatagtt ccatccgacg taaccatccc cgaagacgac 1680
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74 20 25 30
75 Ala Asn His Phe Lys Leu Lys Leu Arg Thr Asp Asp Pro Asn Ser Val
76 35 40 45
77 Lys Leu Leu Glu Arg Tyr Asp Gln Trp Phe Asp Asn Asn Gly Phe Ala
78 50 55 60
79 Lys Leu Leu Ser Ala Arg Met Ala Ser Lys Glu Ser Arg Lys Lys Arg
80 65 70 75 80
81 Lys Asp Glu Ala Ser Thr Ser Asn Thr Thr Lys Arg Thr Arg Ser Gln
82 85 90 95
83 Ala Ser Ile Val Glu Thr Glu Gly Ser Ser Thr Pro Ala Met Pro Ala
84 100 105 110
85 Thr Pro Asn Pro Asp Tyr Leu Asp Pro Arg Leu Ala Asp Ser His Asn
86 115 120 125
87 Asp Asn Gln Gln His Ala Gly Thr Thr Leu Ala Ala Ser Ile Pro Asn
88 130 135 140
89 Gln Leu Pro Thr Ala Asn Ser Ser Ala Lys Thr Arg Thr Gly Pro Thr
90 145 150 155 160
91 Leu Arg Leu Leu Arg Ser Ser Asn Gly Thr Lys Ser Asn Val Leu Pro
92 165 170 175
93 Pro Val Asn Ala Ser Asp Leu Tyr Asp Glu Ser Gln Ser Leu Ala Leu
94 180 185 190
95 Pro Lys Thr Pro Ile Gln Arg Leu His Glu Pro Gly Pro Leu Glu Thr
96 195 200 205
97 Thr Leu Ile Thr Asn Glu Asp Thr Pro Asp Pro Phe Val Asp Ser Gly
98 210 215 220
99 Asp Gln Thr Gln Ala Ser Ala Glu Ala Glu Met Asp Lys Thr Arg Ala
100 225 230 235 240
101 Glu Glu Ile Ser Arg Leu Lys Gly Val Leu Tyr Pro Gly Met Asp Ile
102 245 250 255
103 Phe Asp Ser Ala Thr Val Gln Met Arg Arg Arg Arg Asn Gln Lys Lys

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110 Pro Ser Glu Gln Val Tyr Ser Pro Gly Gly Thr Leu Leu Thr Glu Arg
111          290          295          300
112 Met Ile Thr Gly Asn Val Glu Asp Tyr Ser Pro Leu Lys Gly Glu Thr
113 305          310          315          320
114 Pro Ile Pro Lys Gly Gly Leu Thr Arg Thr Arg Ser Thr Arg Leu Thr
115          325          330          335
116 Lys Ala Asp Pro Asn Val Ser Arg Ala Ala Asp Arg Lys Arg Gln Lys
117          340          345          350
118 Thr Asp Lys Asp Arg Lys Asn Met Ala Asp Glu Gly Ala Asn Glu Glu
119          355          360          365
120 His Thr Ser Ser Arg Arg Ser Arg Arg Ala Ala Ala His Ser Tyr Val
121          370          375          380
122 Gly Asp Asp Glu Glu Ile Gly Leu Thr Val Asn Thr Phe Gly Lys Arg
123 385          390          395          400
124 Pro Arg Gly Gly Phe Asp Val Phe Val Asp Glu Arg Lys Glu Glu Glu
125          405          410          415
126 Asp Ser Lys Thr Thr Tyr Gln Gln Pro Gly Phe Arg Ala Gln Phe Asp
127          420          425          430
128 Thr Leu Thr Pro Thr Arg Leu Val Leu Asn Gly Lys Thr Asn Ala Gly
129          435          440          445
130 Ile His Ala Pro Arg Ile Gly His Ala Ser Leu Ala Lys Glu Asn Ile
131          450          455          460
132 Glu Pro Ile Leu Asn Pro Gln Gly Arg Ile Ala Pro His Gly Trp Asn
133 465          470          475          480
134 Ser Pro Phe Val Lys Tyr Pro Asp Ser Asp Asp Phe Gly Phe Gly Pro
135          485          490          495
136 Ser Tyr Leu Pro Asp Leu Gly Asp Thr Tyr Asp Thr Leu Asp Lys Ala
137          500          505          510
138 Gly Tyr Arg Ser Asn Pro Leu Gln Ala Pro Ser Lys His Pro Phe Tyr
139          515          520          525
140 Glu Ser Gln Tyr Glu Glu Glu His Thr Ala Ala Gln Asn Gly Trp Leu
141          530          535          540
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159 atcaaggtct ttgcgcgcag tcccggtcag agcacggacg agtacacaaa acaagtcaat 180

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162 cactccctga tcacggctgg tccctcgcac agattaccct cggaagaggc agactgtctt 360
163 ttcaagcagc ttcttcgtgg catctcctac cttcacaat caggcatcgc ccaccgcgac 420
164 ctgaagccgg agaacctcct cctgacacac agggcttgcc tcaagatctc agactttgcg 480
165 aatgccgagc gcgtccgttt cgatggtgat gattctcagc atgccaatga cctggcggaa 540
166 actgaacgcc gcagcttaga accgacaccg tatcttgccc cggagcgata ccttgacgag 600
167 ggcgacaggt acatgtccag atccgacccc agagccctcg atatctgggc cgcggctgtt 660
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169 ggcttcaggg cgtatgtcga agagcgtaag gccgagaaga cgaatactgt tatccaggat 780
170 tcgtgccatg aacggggccg caaagtata tacgccatgt taagcactga tcctggggaag 840
171 cgacctatcg cgactgagat tctttcctca gagtggcttc agaacattga ctgctgtatc 900
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187 Pro Pro Leu Asp Arg Tyr Tyr Ala Ile Lys Val Phe Arg Arg Ser Pro
188 35 40 45
189 Gly Gln Ser Thr Asp Glu Tyr Thr Lys Gln Val Asn Ala Glu Phe Ala
190 50 55 60
191 Val Val Ala Asn Leu His Gln His Val Val Ser Thr Phe Glu Leu
192 65 70 75 80
193 Leu Pro Ile Gly Gly Gly Asn Leu Ala Ala Cys Met Glu Tyr Cys Ala
194 85 90 95
195 Gly Gly Asp Leu His Ser Leu Ile Thr Ala Gly Pro Ser His Arg Leu
196 100 105 110
197 Pro Ser Glu Glu Ala Asp Cys Leu Phe Lys Gln Leu Leu Arg Gly Ile
198 115 120 125
199 Ser Tyr Leu His Lys Ser Gly Ile Ala His Arg Asp Leu Lys Pro Glu
200 130 135 140
201 Asn Leu Leu Leu Thr His Arg Ala Cys Leu Lys Ile Ser Asp Phe Ala
202 145 150 155 160
203 Asn Ala Glu Arg Val Arg Phe Asp Gly Asp Asp Ser Gln His Ala Asn
204 165 170 175
205 Asp Leu Ala Glu Thr Glu Arg Arg Ser Leu Glu Pro Thr Pro Tyr Leu
206 180 185 190
207 Ala Pro Glu Arg Tyr Leu Asp Glu Gly Asp Arg Tyr Met Ser Arg Ser
208 195 200 205
209 Asp Pro Arg Ala Leu Asp Ile Trp Ala Ala Ala Val Ile Tyr Val Ala
210 210 215 220
211 Met Arg Thr Gly Arg Asn Leu Trp Lys Ala Ala Thr Glu Lys Asp Glu

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212 225          230          235          240
213 Gly Phe Arg Ala Tyr Val Glu Glu Arg Lys Ala Glu Lys Thr Asn Thr
214          245          250          255
215 Val Ile Gln Asp Ser Cys His Glu Arg Gly Arg Lys Val Ile Tyr Ala
216          260          265          270
217 Met Leu Ser Thr Asp Pro Gly Lys Arg Pro Ile Ala Thr Glu Ile Leu
218          275          280          285
219 Ser Ser Glu Trp Leu Gln Asn Ile Asp Cys Cys Ile Phe Asp His Ser
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236 tacttagcca tgcagttcga tcccagcaaa cccggtgctc gagaccctt tggccgaact 180
237 ggcggatacg gagcaaatgg tgcataccct aatgagccaa caccttcagg caaagtgtgtg 240
238 atccatcact ttacctgtcg atccctgaca attggcagct ggaggcggat cggacaaaat 300
239 gccatggacc tggttgtttt ctactcccc gagaggcgt gcatgacct ctatatcaac 360
240 aacgacgcag ccgatacaa aatcgaatat cccttctcct acatcaagaa cattacactt 420
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VERIFICATION SUMMARY

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Input Set : A:\MIC-004.ST25.txt

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